

SEQUENCE LISTING

SEQUENCE LISTING

<110> SISODIA, SANGRAM S.
YU, CHUNJIANG

<120> MEMBRANE PREPARATION FROM PICHIA PASTORIS TO ASSAY
Y-SECRETASE ACTIVITY

<130> ARCD:398WO

<141> PCT/US2004/031230
<141> 2004-09-23

<150> 10/948,629
<151> 2004-09-23

<150> 60/505,601
<151> 2003-09-23

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 2763
<212> DNA
<213> Homo sapiens

<400> 1
 tgggacaggc agctccgggg tccgcgggtt cacatcggaa acaaaacagc ggctggtctg 60
 gaaggaacct gagctacgag ccgcggcggc agcggggcgg cggggaagcg tatacctaata 120
 ctgggagcct gcaagtgcaca acagcctttg cggtccttag acagcttggc ctggaggaga 180
 acacatgaaa gaaagaacct caagaggcct tgttttctgt gaaacagtat ttctatacag 240
 ttgctccaat gacagagtta cctgcaccgt tgtcctactt ccagaatgca cagatgtctg 300
 aggacaacca cctgagcaat actgtacgta gccagaatga caatagagaa cggcaggagc 360
 acaacgacag acggagcctt ggccaccctg agccattatc taatggacga cccagggta 420
 actcccggca ggtggtggag caagatgagg aagaagatga ggagctgaca ttgaaatatg 480
 gcgccaagca tgtgatcatg ctctttgtcc ctgtgactct ctgcatggtg gtggtcgtgg 540
 ctaccattaa gtcagtcagc ttttataccc ggaaggatgg gcagctaata tatacccat 600
 tcacagaaga taccgagact gtgggccaga gagccctgca ctcaattctg aatgctgcca 660
 tcatgatcag tgtcattgtt gtcatgacta tcctcctggt ggttctgtat aaatacaggt 720
 gctataaggt catccatgcc tggcttatta tatcatctct attgttgctg ttcttttttt 780
 cattcattta cttgggggaa gtgtttaaaa cctataacgt tgctgtggac tacattactg 840
 ttgcaactct gatctggaat tttggtgtgg tgggaatgat ttccattcac tggaaaggtc 900
 cacttcgact ccagcaggca tatctcatta tgattagtgc cctcatggcc ctggtgttta 960
 tcaagtacct ccctgaatgg actgcgtggc tcatcttggc tgtgatttca gtatatgatt 1020
 tagtggtgtg tttgtgtccg aaagggtccac ttcgtatgct ggttgaaaca gctcaggaga 1080
 gaaatgaaac gctttttcca gctctcattt actcctcaac aatggtgtgg ttggtgaata 1140
 tggcagaagg agaccgggaa gctcaaagga gagtatccaa aaattccaag tataatgcag 1200
 aaagcacaga aaggagatca caagacactg ttgcagagaa tgatgatggc ggggttcagt 1260
 aggaatggga agcccagagg gacagtcacg tagggcctca tcgctctaca cctgagtcac 1320
 gagctgctgt ccaggaactt tccagcaact tcctcgctgg tgaagacca gaggaagg 1380
 gagtaaaact tggattggga gatttcattt tctacagtgt tctggttggt aaagcctcag 1440
 caacagccag tggagactgg aacacaacca tagcctgtt cgtagccata ttaattggtt 1500
 tgtgccttac attattactc cttgccattt tcaagaaagc attgccagct cttccaatct 1560
 ccatcacctt tgggcttggt ttctactttg ccacagatta tcttgtacag ctttttatgg 1620
 accaattagc attccatcaa ttttatatct agcatatttg cggttagaat cccatggatg 1680
 tttcttcttt gactataaca aaatctgggg aggacaaagg tgattttcct gtgtccacat 1740
 ctaacaaagt caagattccc ggctggactt ttgcagcttc cttccaagtc ttctgacca 1800

```

ccttgcaacta ttggactttg gaaggaggtg cctatagaaa acgattttga acataacttca 1860
tcgcagtggga ctgtgtccct cgggtgcagaa actaccagat ttgagggacg aggtcaagga 1920
gatatgatag gcccggaagt tgctgtgccc catcagcagc ttgacgcgtg gtcacaggac 1980
gatttcactg acactgcgaa ctctcaggac taccgttacc aagagggttag gtgaagtggg 2040
ttaaaccaaaa cggaactctt catcttaaac tacacgttga aaatcaaccc aataattctg 2100
tattaactga attctgaact tttcaggagg tactgtgagg aagagcaggc accagcagca 2160
gaatgggggaa tggagaggtg ggcagggggt ccagcttccc tttgattttt tgctgcagac 2220
tcctcctttt taaatgagac ttgttttccc ctctctttga gtcaagtcaa atatgtagat 2280
tgccttttggc aattcttctt ctcaagcact gacactcatt accgtctgtg attgccattt 2340
cttcccaagg ccagtctgaa cctgaggttg ctttataccta aaagttttaa cctcagggtt 2400
caaattcagt aaatttttgg aacagtacag ctattttctc tcaattctct atcatgttga 2460
agtcaaattt ggattttcca ccaaattctg aatttgtaga cataacttga cgctcacttg 2520
ccccagatgc ctctctgtgc ctctcttctt tctcccacac aagcagtctt tttctacagc 2580
cagtaaggca gctctgtcgt ggtagcagat ggtcccatTA ttctagggtc ttactctttg 2640
tatgatgaaa agaattgtgt atgaatcggt gctgtcagcc ctgctgtcag accttcttcc 2700
acagcaaattg agatgtatgc ccaaagcggg agaattaaag aagagtaaaa tggctgttga 2760
agc

```

<210> 2

<211> 467

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
  1                      5                      10                      15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
      20                      25                      30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
      35                      40                      45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
      50                      55                      60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
      65                      70                      75                      80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
      85                      90                      95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
      100                      105                      110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
      115                      120                      125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
      130                      135                      140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
      145                      150                      155                      160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
      165                      170                      175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
      180                      185                      190

```

Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val		
	195						200					205					
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala		
	210					215					220						
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr		
	225				230					235					240		
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr		
				245					250					255			
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	Arg	Met	Leu	Val		
			260					265					270				
Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	Ile	Tyr		
		275					280					285					
Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	Pro	Glu		
	290					295					300						
Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	Tyr	Asn	Ala	Glu	Ser	Thr		
	305				310					315					320		
Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	Gly	Phe		
				325					330					335			
Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	His	Arg		
			340					345					350				
Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	Ser	Ile		
		355					360					365					
Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly		
	370					375					380						
Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	Thr	Ala		
	385				390					395					400		
Ser	Gly	Asp	Trp	Asn	Thr	Thr	Ile	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile		
				405					410					415			
Gly	Leu	Cys	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Phe	Lys	Lys	Ala	Leu		
			420					425					430				
Pro	Ala	Leu	Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Val	Phe	Tyr	Phe	Ala		
		435					440					445					
Thr	Asp	Tyr	Leu	Val	Gln	Pro	Phe	Met	Asp	Gln	Leu	Ala	Phe	His	Gln		
	450					455					460						
Phe	Tyr	Ile															
	465																

<210> 3

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 3
ggcgaattca ccatgggggc tgcggtgt 28

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 4
ggcgaattct caatgggtgat ggtgatgatg 30

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 5
gcccaattga ccatgggtac ggcaggggggt 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 6
gcccaattgt cagtatgaca cagctcctgg 30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
ggcgaattca ccatgaacct ggagcgagtg 30

<210> 8
<211> 30

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

 <400> 8
 ggcgaattct cagggggtgc ccaggggtat 30

 <210> 9
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <400> 9
 tctctcgaga aaagagatgc agaattccga catgac 36

 <210> 10
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

 <400> 10
 ggctctagac cggttctgcat ctgctcaaag aac 33

 <210> 11
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

 <400> 11
 gccagatctc atcttgtgac tggttgatc 29

 <210> 12
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 Primer

 <400> 12
 cgcgatccg tagtaccgtc aaatatcatc 30

 <210> 13
 <211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 13
cgcggatcca ggtagtgaag atgtagag 28

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
ggcagatctg agccatactt ccaactatc 29

<210> 15
<211> 297
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 15
gatgcagaat tccgacatga ctcaggatat gaagttcatc atcaaaaatt ggtgttcttt 60
gcagaagatg tgggttcaaa caaagggtgca atcattggac tcatggtggg cgggtgttgtc 120
atagcgacag tgatcgatc cacttggtg atgctgaaga agaaacagta cacatccatt 180
catcatgggt tgggtggagg tgacgccgct gtcaccccag aggagcgcca cctgtccaag 240
atgcagcaga acggctacga aaatccaacc tacaagttct ttgagcagat gcagaac 297

<210> 16
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Peptide

<400> 16
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
1 5 10 15
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu

50					55					60					
Phe 65	Ile	Asn	Thr	Thr	Ile 70	Ala	Ser	Ile	Ala	Ala 75	Lys	Glu	Glu	Gly	Val 80
Ser	Leu	Glu	Lys	Arg 85	Asp	Ala	Glu	Phe	Arg 90	His	Asp	Ser	Gly	Tyr 95	Glu
Val	His	His	Gln 100	Lys	Leu	Val	Phe	Phe 105	Ala	Glu	Asp	Val	Gly 110	Ser	Asn
Lys	Gly	Ala 115	Ile	Ile	Gly	Leu	Met 120	Val	Gly	Gly	Val	Val 125	Ile	Ala	Thr
Val 130	Ile	Val	Ile	Thr	Leu	Val 135	Met	Leu	Lys	Lys	Lys 140	Gln	Tyr	Thr	Ser
Ile 145	His	His	Gly	Val	Val 150	Glu	Val	Asp	Ala	Ala 155	Val	Thr	Pro	Glu	Glu 160
Arg	His	Leu	Ser	Lys 165	Met	Gln	Gln	Asn	Gly 170	Tyr	Glu	Asn	Pro	Thr 175	Tyr
Lys	Phe	Phe	Glu 180	Gln	Met	Gln	Asn	Gly 185	Leu	Glu	Gln	Lys	Leu 190	Ile	Ser
Glu	Glu	Asp 195	Leu	Asn	Ser	Ala	Val 200	Asp	His	His	His	His 205	His	His	